	Type	Hits	Search Text	DBs
1	BRS	1515	BAKER-KEVIN-P	USPAT; US-PGPUB; EPO; JPO; DERWENT
2	BRS	374	BOTSTEIN-DAVID	USPAT; US-PGPUB; EPO; JPO; DERWENT
3	BRS	1420	DESNOYERS-LUC	USPAT; US-PGPUB; EPO; JPO; DERWENT
4	BRS	415	FERRARA-NAPOLEONE	USPAT; US-PGPUB; EPO; JPO; DERWENT
5	BRS	482	FONG-SHERMAN	USPAT; US-PGPUB; EPO; JPO; DERWENT
6	BRS	713	GAO-WEI-QIANG	USPAT; US-PGPUB; EPO; JPO; DERWENT
7	BRS	1870	GODDARD-AUDREY	USPAT; US-PGPUB; EPO; JPO; DERWENT
8	BRS	1689	GODOWSKI-PAUL-J	USPAT; US-PGPUB; EPO; JPO; DERWENT
9	BRS	718	GRIMALDI-J-CHRISTOPHER	USPAT; US-PGPUB; EPO; JPO; DERWENT
10	BRS	1837	GURNEY-AUSTIN-L	USPAT; US-PGPUB; EPO; JPO; DERWENT
11	BRS	302	HILLAN-KENNETH-J	USPAT; US-PGPUB; EPO; JPO; DERWENT
12	BRS	903	PAN-JAMES	USPAT; US-PGPUB; EPO; JPO; DERWENT
13	BRS	337	PAONI-NICHOLAS-F	USPAT; US-PGPUB; EPO; JPO; DERWENT
14	BRS	364	ROY-MARGARET-ANN	USPAT; US-PGPUB; EPO; JPO; DERWENT
15	BRS	1270	SMITH-VICTORIA	USPAT; US-PGPUB; EPO; JPO; DERWENT
16	BRS	804	STEWART-TIMOTHY-A	USPAT; US-PGPUB; EPO; JPO; DERWENT
17	BRS	832	TUMAS-DANIEL	USPAT; US-PGPUB; EPO; JPO; DERWENT
18	BRS	1558	WATANABE-COLIN-K	USPAT; US-PGPUB; EPO; JPO; DERWENT
19	BRS	353	WILLIAMS-P-MICKEY	USPAT; US-PGPUB; EPO; JPO; DERWENT
20	BRS	1906	WOOD-WILLIAM-I	USPAT; US-PGPUB; EPO; JPO; DERWENT
21	BRS	73	PRO1759	USPAT; US-PGPUB; EPO; JPO; DERWENT

10/020,063

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Set       Items     Description
S1          5       PRO1759
S2        333       RD (unique items)
S3          5       AU='BAKER, KEVIN P'
S4         12       AU='BAKER KEVIN P'
S5       1526       AU='BAKER K P'
S6         86       AU='BOTSTEIN, DAVID'
S7        250       AU='BOTSTEIN DAVID'
S8         12       AU='DESNOYERS, L.'
S9       1388       AU='DESNOYERS L'
S10         9       AU='DESNOYERS LUC'
S11        22       AU='DESNOYERS L.'
S12        18       AU='FERRARA, NAPOLEONE'
S13      1211       AU='FERRARA N'
S14         2       AU='FONG, SHERMAN'
S15        31       AU='FONG SHERMAN'
S16         8       AU='GAO, WEI-QIANG'
S17        56       AU='GAO WEI-QIANG'
S18        13       AU='GODDARD, A.'
S19         6       AU='GODDARD, AUDREY'
S20      1999       AU='GODDARD A'
S21        53       AU='GODDARD AUDREY'
S22        12       AU='GODOWSKI, PAUL J'
S23        85       AU='GODOWSKI PAUL J'
S24         3       AU='GRIMALDI, J. CHRISTOPHER'
S25        25       AU='GRIMALDI J CHRISTOPHER'
S26       698       AU='GRIMALDI J C'
S27        12       AU='GURNEY, A. L.'
S28        13       AU='GURNEY, AUSTIN L'
S29      1775       AU='GURNEY A L'
S30        58       AU='GURNEY AUSTIN L'
S31       375       AU='HILLAN K J'
S32        59       AU='HILLAN K.J.'
S33        35       AU='HILLAN KENNETH J'
S34         2       AU='PAN, JAMES'
S35         8       AU='PAN JAMES'
S36         4       AU='PAONI, NICHOLAS F'
S37        42       AU='PAONI NICHOLAS F'
S38        42       AU='PAONI NF'
S39         1       AU='ROY, MARGARET A'
S40        12       AU='ROY, M. A.'
S41         5       AU='ROY MARGARET ANN'
S42       465       AU='ROY M A'
S43         7       AU='SMITH, VICTORIA'
S44        16       AU='SMITH VICTORIA'
S45         4       AU='STEWART, TIMOTHY A'
S46        16       AU='STEWART, S. A.'
S47        41       AU='STEWART TIMOTHY A'
S48       109       AU='STEWART TA'
S49        15       AU='TUMAS DANIEL'
S50       811       AU='TUMAS D'
S51         2       AU='WATANABE, COLIN K'
S52         2       AU='WATANABE COLIN K'
S53      1474       AU='WATANABE C K'
S54         2       AU='WATANABE C.K.'
S55       388       AU='WILLIAMS, P. M.'
S56       814       AU='WILLIAMS P M'
S57        35       AU='WILLIAMS P MICKEY'
S58       163       AU='WILLIAMS P.M.'
S59        11       AU='WOOD, WILLIAM I'
S60        64       AU='WOOD WILLIAM I'
?
```

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OM nucleic - nucleic search, using sw model

Run on: August 6, 2004, 22:05:41 ; Search time 672 Seconds
                                               (without alignments)
                                               10784.860 Million cell updates/sec

Title: US-10-020-063A-373
Perfect score: 1706
Sequence: 1 ggagcgctgctggaacccga..........aaatgatcaaaaaaaaaaaa 1706

Scoring table: IDENTITY_NUC
                   Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   N_Geneseq_29Jan04:*
                   1: geneseqn1980s:*
                   2: geneseqn1990s:*
                   3: geneseqn2000s:*
                   4: geneseqn2001as:*
                   5: geneseqn2001bs:*
                   6: geneseqn2002s:*
                   7: geneseqn2003as:*
                   8: geneseqn2003bs:*
                   9: geneseqn2003cs:*
                   10: geneseqn2004s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1706	100.0	1706	3	AAA37130	Aaa37130 Human PRO
2	1706	100.0	1706	4	AAF54464	Aaf54464 Probe # 7
3	1706	100.0	1706	6	ABK40268	Abk40268 cDNA enco
4	1706	100.0	1706	8	ACD68503	Acd68503 Novel hum
5	1706	100.0	1706	8	ACH04605	Ach04605 Human cDN
6	1706	100.0	1706	8	ACD68149	Acd68149 Novel hum
7	1706	100.0	1706	9	ADC18242	Adc18242 Human PRO

	8	1706	100.0	1706	9	ADD70888	Add70888 Human cDN
	9	1706	100.0	1706	9	ADD39965	Add39965 Human cDN
	10	1706	100.0	1706	9	ADD70411	Add70411 Human cDN
	11	1706	100.0	1706	9	ADD38532	Add38532 Human cDN
	12	1706	100.0	1706	9	ADD39488	Add39488 Human cDN
	13	1706	100.0	1706	9	ADD39011	Add39011 Human cDN
	14	1706	100.0	1706	9	ADD40442	Add40442 Human cDN
	15	1706	100.0	1706	9	ADE50663	Ade50663 Human cDN
	16	1706	100.0	1706	9	ADE20275	Ade20275 Human cDN
	17	1706	100.0	1706	9	ADE50186	Ade50186 Human cDN
	18	1706	100.0	1706	9	ADE21744	Ade21744 Human cDN
	19	1706	100.0	1859	9	ADD19230	Add19230 Human cDN
	20	1704.4	99.9	1765	4	AAI58814	Aai58814 Human pol
	21	1704.4	99.9	1765	8	ADB48795	Adb48795 Novel hum
	22	1702.4	99.8	1763	4	AAI60600	Aai60600 Human pol
	23	1689.8	99.1	1761	4	AAK94208	Aak94208 Human ful
	24	1685.4	98.8	1730	3	AAZ98171	Aaz98171 Human sig
	25	1599.8	93.8	1688	6	ABK34655	Abk34655 Human cDN
	26	1562.6	91.6	1715	2	AAZ00839	Aaz00839 Human sec
	27	1351.4	79.2	1353	5	AAH52165	Aah52165 Human AFP
	28	594	34.8	594	9	ADD19231	Add19231 Human cDN
	29	552	32.4	694	4	AAK93759	Aak93759 Human cDN
	30	552	32.4	694	4	AAK91739	Aak91739 Human cDN
	31	527.6	30.9	543	9	ADD19192	Add19192 Human cDN
c	32	473	27.7	541	4	AAK92556	Aak92556 Human cDN
	33	423.8	24.8	454	8	ACH15269	Ach15269 Human adu
	34	403.8	23.7	407	8	ACH19059	Ach19059 Human adu
	35	373.6	21.9	404	2	AAQ61193	Aaq61193 Human bra
	36	285.6	16.7	324	6	ABK38904	Abk38904 cDNA enco
	37	285.6	16.7	324	7	ACA11233	Aca11233 Human lun
	38	285.6	16.7	324	7	ACA02419	Aca02419 Lung canc
	39	160.2	9.4	1760	3	AAC44674	Aac44674 Zea mays
	40	151.8	8.9	157	2	AAT21987	Aat21987 Human gen
	41	147.4	8.6	1878	3	AAC44133	Aac44133 Zea mays
	42	145.8	8.5	1822	3	AAC48019	Aac48019 Zea mays
	43	127.2	7.5	1536	3	AAC51479	Aac51479 Arabidops
	44	126	7.4	1646	3	AAC40303	Aac40303 Arabidops
	45	124.8	7.3	1425	3	AAC51467	Aac51467 Arabidops
	46	124.2	7.3	1649	3	AAC47064	Aac47064 Arabidops
	47	110.8	6.5	803	3	AAC52186	Aac52186 Arabidops
	48	95.8	5.6	1263	3	AAC43008	Aac43008 Arabidops
	49	95.8	5.6	1263	6	ABZ13231	Abz13231 Arabidops
	50	95.8	5.6	1698	3	AAC36256	Aac36256 Arabidops
c	51	53.2	3.1	10732	3	AAA10594	Aaa10594 Gene enco
	52	52.8	3.1	306	6	ABL75746	Abl75746 Corn tass
c	53	52.6	3.1	2000	7	ADA71938	Ada71938 Rice gene
	54	49.2	2.9	451	3	AAC52952	Aac52952 Arabidops
	55	45.6	2.7	2000	7	ADA71938	Ada71938 Rice gene
c	56	44.8	2.6	2252	4	ABL21923	Abl21923 Drosophil
	57	44.8	2.6	4600	4	ABL21922	Abl21922 Drosophil
	58	44.4	2.6	68230	8	ADA66349	Ada66349 Mouse Ppp
	59	44.4	2.6	68233	8	ADA03065	Ada03065 Mouse Ppp
	60	44.4	2.6	68233	9	ADB72803	Adb72803 Mouse Ppp
	61	43	2.5	15935	4	ABL06114	Abl06114 Drosophil
c	62	42.6	2.5	3489	3	AAA30290	Aaa30290 Kaposi's
c	63	42.6	2.5	3489	4	AAF82901	Aaf82901 Nucleotid
c	64	42.6	2.5	3489	6	ABA93487	Aba93487 Kaposi's

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OM nucleic - nucleic search, using sw model

Run on:          August  6, 2004, 23:01:32 ; Search time 6544 Seconds
                                          (without alignments)
                                          11299.391 Million cell updates/sec

Title:           US-10-020-063A-373
Perfect score:   1706
Sequence:        1 ggagcgctgctggaacccga..........aaatgatcaaaaaaaaaaaa 1706

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters:      6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :       GenEmbl:*
                 1:   gb_ba:*
                 2:   gb_htg:*
                 3:   gb_in:*.
                 4:   gb_om:*
                 5:   gb_ov:*
                 6:   gb_pat:*
                 7:   gb_ph:*
                 8:   gb_pl:*
                 9:   gb_pr:*
                 10:  gb_ro:*
                 11:  gb_sts:*
                 12:  gb_sy:*
                 13:  gb_un:*
                 14:  gb_vi:*
                 15:  em_ba:*
                 16:  em_fun:*
                 17:  em_hum:*
                 18:  em_in:*
                 19:  em_mu:*
                 20:  em_om:*
                 21:  em_or:*
                 22:  em_ov:*
                 23:  em_pat:*
                 24:  em_ph:*
                 25:  em_pl:*
                 26:  em_ro:*
                 27:  em_sts:*
```

```
28:  em_un:*
29:  em_vi:*
30:  em_htg_hum:*
31:  em_htg_inv:*
32:  em_htg_other:*
33:  em_htg_mus:*
34:  em_htg_pln:*
35:  em_htg_rod:*
36:  em_htg_mam:*
37:  em_htg_vrt:*
38:  em_sy:*
39:  em_htgo_hum:*
40:  em_htgo_mus:*
41:  em_htgo_other:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1706	100.0	1706	6	AX201350	AX201350 Sequence
	2	1706	100.0	1706	6	AX697305	AX697305 Sequence
	3	1706	100.0	1706	9	AY358604	AY358604 Homo sapi
	4	1706	100.0	1859	6	AR339787	AR339787 Sequence
	5	1704.4	99.9	1765	6	AR339214	AR339214 Sequence
	6	1689.8	99.1	1761	6	BD127237	BD127237 Primer fo
	7	1689.8	99.1	1761	9	AK074684	AK074684 Homo sapi
	8	1685.4	98.8	1730	6	BD222717	BD222717 Human sig
	9	1663	97.5	1675	9	HSM806703	BX640649 Homo sapi
c	10	1590.4	93.2	55034	9	AC021072	AC021072 Homo sapi
	11	1589.8	93.2	1598	9	BC007703	BC007703 Homo sapi
	12	1562.6	91.6	1715	6	AR339798	AR339798 Sequence
	13	1562.6	91.6	1715	6	BD131133	BD131133 45 human
	14	1351.4	79.2	1353	6	AX118981	AX118981 Sequence
	15	1136.2	66.6	1673	10	BC009140	BC009140 Mus muscu
	16	1132.8	66.4	138860	2	AC055703	AC055703 Mus muscu
	17	1128	66.1	254686	2	AC097309	AC097309 Rattus no
	18	1022.2	59.9	1694	6	AX834888	AX834888 Sequence
	19	1022.2	59.9	1694	9	AK097576	AK097576 Homo sapi
	20	953.6	55.9	259204	2	AC095370	AC095370 Rattus no
c	21	953.6	55.9	283969	2	AC120737	AC120737 Rattus no
	22	854.2	50.1	189106	2	AC110121	AC110121 Rattus no
	23	703.8	41.3	191947	2	AC135875	AC135875 Rattus no
	24	625.8	36.7	210830	2	AC128971	AC128971 Rattus no
c	25	563.6	33.0	189106	2	AC110121	AC110121 Rattus no
	26	552	32.4	694	6	BD124768	BD124768 Primer fo
	27	552	32.4	694	6	BD126788	BD126788 Primer fo
c	28	473	27.7	541	6	BD125585	BD125585 Primer fo
	29	379.8	22.3	204288	2	BX470261	BX470261 Danio rer
	30	379.8	22.3	214400	2	BX546466	BX546466 Danio rer
	31	379.8	22.3	222308	2	BX465853	BX465853 Danio rer
	32	378.2	22.2	141134	5	BX248228	BX248228 Zebrafish
	33	285.6	16.7	324	6	AR273199	AR273199 Sequence

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OM nucleic - nucleic search, using sw model

Run on: August 6, 2004, 23:00:17 ; Search time 4074 Seconds
                                          (without alignments)
                                          .12504.880 Million cell updates/sec

Title: US-10-020-063A-373
Perfect score: 1706
Sequence: 1 ggagcgctgctggaacccga..........aaatgatcaaaaaaaaaaa 1706

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   EST:*
                 1:   em_estba:*
                 2:   em_esthum:*
                 3:   em_estin:*
                 4:   em_estmu:*
                 5:   em_estov:*
                 6:   em_estpl:*
                 7:   em_estro:*
                 8:   em_htc:*
                 9:   gb_est1:*
                 10: gb_est2:*
                 11: gb_htc:*
                 12: gb_est3:*
                 13: gb_est4:*
                 14: gb_est5:*
                 15: em_estfun:*
                 16: em_estom:*
                 17: em_gss_hum:*
                 18: em_gss_inv:*
                 19: em_gss_pln:*
                 20: em_gss_vrt:*
                 21: em_gss_fun:*
                 22: em_gss_mam:*
                 23: em_gss_mus:*
                 24: em_gss_pro:*
                 25: em_gss_rod:*
                 26: em_gss_phg:*
                 27: em_gss_vrl:*

```
28:  gb_gss1:*
29:  gb_gss2:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

<div align="center">SUMMARIES</div>

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1351.4	79.2	1353	29	AY404433	AY404433 Homo sapi
	2	1210.8	71.0	1745	11	AK089268	AK089268 Mus muscu
	3	1188.8	69.7	1747	11	AK087550	AK087550 Mus muscu
	4	1134.8	66.5	1169	29	AY404434	AY404434 Pan trogl
	5	1093.8	64.1	1353	29	AY404435	AY404435 Mus muscu
	6	985	57.7	1201	9	AL534846	AL534846 AL534846
c	7	956.8	56.1	1201	9	AL565683	AL565683 AL565683
c	8	945	55.4	1019	9	AL582149	AL582149 AL582149
c	9	930.2	54.5	1201	9	AL578311	AL578311 AL578311
	10	925.6	54.3	1201	9	AL529419	AL529419 AL529419
	11	920	53.9	1201	9	AL556349	AL556349 AL556349
c	12	903	52.9	931	9	AL570277	AL570277 AL570277
c	13	901.2	52.8	1043	9	AL552603	AL552603 AL552603
	14	893.8	52.4	1201	13	BX426466	BX426466 BX426466
	15	893.6	52.4	1201	13	BX376703	BX376703 BX376703
c	16	885	51.9	990	13	BX325317	BX325317 BX325317
	17	876.8	51.4	987	12	BM809047	BM809047 AGENCOURT
c	18	873.8	51.2	921	9	AL528940	AL528940 AL528940
	19	868	50.9	1028	9	AL552646	AL552646 AL552646
c	20	863.8	50.6	1201	9	AL578632	AL578632 AL578632
	21	851.4	49.9	991	13	BX402893	BX402893 BX402893
	22	850.4	49.8	931	9	AL528941	AL528941 AL528941
c	23	848.6	49.7	957	9	AL580492	AL580492 AL580492
	24	848	49.7	976	13	BX325318	BX325318 BX325318
	25	845.4	49.6	1201	9	AL555944	AL555944 AL555944
c	26	842	49.4	1005	13	BX402892	BX402892 BX402892
	27	837.2	49.1	919	12	BI837146	BI837146 603089918
c	28	833.8	48.9	1201	9	AL529418	AL529418 AL529418
	29	819.8	48.1	1201	9	AL554939	AL554939 AL554939
c	30	816.2	47.8	1201	9	AL577536	AL577536 AL577536
	31	812.6	47.6	1046	13	BQ072939	BQ072939 AGENCOURT
c	32	811.4	47.6	899	13	BX350824	BX350824 BX350824
	33	805	47.2	833	12	BI916174	BI916174 603178058
	34	797.4	46.7	844	12	BI915575	BI915575 603176933
	35	795.4	46.6	1060	13	BU157288	BU157288 AGENCOURT
	36	792.8	46.5	798	14	CF127419	CF127419 UI-HF-ET0
c	37	786.2	46.1	1245	10	BF690150	BF690150 602186478
	38	786	46.1	865	12	BI770187	BI770187 603053218
c	39	784.2	46.0	1201	13	BX426465	BX426465 BX426465
	40	781.6	45.8	857	12	BI914370	BI914370 603182368
	41	769.2	45.1	942	9	AL558736	AL558736 AL558736
	42	764.8	44.8	795	12	BM015349	BM015349 603641509
	43	757.4	44.4	953	9	AL544036	AL544036 AL544036
	44	754	44.2	845	13	BU509556	BU509556 AGENCOURT
	45	749	43.9	859	12	BI601017	BI601017 603247386

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OM nucleic - nucleic search, using sw model

Run on: August 6, 2004, 23:07:42 ; Search time 796 Seconds
                                            (without alignments)
                                            10508.489 Million cell updates/sec

Title: US-10-020-063A-373
Perfect score: 1706
Sequence: 1 ggagcgctgctggaacccga.........aaatgatcaaaaaaaaaaaa 1706

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 3222919 seqs, 2451570024 residues

Total number of hits satisfying chosen parameters: 6445838

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   Published_Applications_NA:*
            1:   /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
            2:   /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
            3:   /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
            4:   /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
            5:   /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
            6:   /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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            8:   /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
            9:   /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
           10:   /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
           11:   /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
           12:   /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
           13:   /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
           14:   /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
           15:   /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
           16:   /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
           17:   /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
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           19:   /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

         Pred. No. is the number of results predicted by chance to have a
         score greater than or equal to the score of the result being printed,
         and is derived by analysis of the total score distribution.

                               SUMMARIES
                         %
Result   Query

No.	Score	Match	Length	DB	ID	Description
1	1706	100.0	1706	10	US-09-946-374-373	Sequence 373, App
2	1706	100.0	1706	12	US-10-015-395A-373	Sequence 373, App
3	1706	100.0	1706	13	US-10-006-485A-373	Sequence 373, App
4	1706	100.0	1706	13	US-10-013-907A-373	Sequence 373, App
5	1706	100.0	1706	13	US-10-015-499A-373	Sequence 373, App
6	1706	100.0	1706	13	US-10-211-858-29	Sequence 29, Appl
7	1706	100.0	1706	13	US-10-226-254A-373	Sequence 373, App
8	1706	100.0	1706	15	US-10-006-856A-373	Sequence 373, App
9	1706	100.0	1706	15	US-10-006-818A-373	Sequence 373, App
10	1706	100.0	1706	15	US-10-015-393A-373	Sequence 373, App
11	1706	100.0	1706	15	US-10-015-869A-373	Sequence 373, App
12	1706	100.0	1706	15	US-10-012-121A-373	Sequence 373, App
13	1706	100.0	1706	15	US-10-006-116A-373	Sequence 373, App
14	1706	100.0	1706	15	US-10-006-117A-373	Sequence 373, App
15	1706	100.0	1706	15	US-10-017-527A-373	Sequence 373, App
16	1706	100.0	1706	15	US-10-013-913A-373	Sequence 373, App
17	1706	100.0	1706	15	US-10-007-194A-373	Sequence 373, App
18	1706	100.0	1706	15	US-10-013-430A-373	Sequence 373, App
19	1706	100.0	1706	15	US-10-011-671A-373	Sequence 373, App
20	1706	100.0	1706	15	US-10-012-755A-373	Sequence 373, App
21	1706	100.0	1706	15	US-10-015-386A-373	Sequence 373, App
22	1706	100.0	1706	15	US-10-011-692A-373	Sequence 373, App
23	1706	100.0	1706	15	US-10-006-768A-373	Sequence 373, App
24	1706	100.0	1706	15	US-10-017-610A-373	Sequence 373, App
25	1706	100.0	1706	15	US-10-006-063A-373	Sequence 373, App
26	1706	100.0	1706	15	US-10-020-063A-373	Sequence 373, App
27	1706	100.0	1706	15	US-10-015-391A-373	Sequence 373, App
28	1706	100.0	1706	15	US-10-017-407A-373	Sequence 373, App
29	1706	100.0	1706	15	US-10-011-833A-373	Sequence 373, App
30	1706	100.0	1706	15	US-10-006-041A-373	Sequence 373, App
31	1706	100.0	1706	15	US-10-015-822A-373	Sequence 373, App
32	1706	100.0	1706	15	US-10-015-387A-373	Sequence 373, App
33	1706	100.0	1706	15	US-10-006-130A-373	Sequence 373, App
34	1706	100.0	1706	15	US-10-006-172A-373	Sequence 373, App
35	1706	100.0	1706	15	US-10-017-253A-373	Sequence 373, App
36	1706	100.0	1706	15	US-10-015-392A-373	Sequence 373, App
37	1706	100.0	1706	15	US-10-210-951-29	Sequence 29, Appl
38	1706	100.0	1706	15	US-10-017-306A-373	Sequence 373, App
39	1706	100.0	1706	15	US-10-211-884-29	Sequence 29, Appl
40	1706	100.0	1706	15	US-10-017-867A-373	Sequence 373, App
41	1706	100.0	1706	15	US-10-012-064A-373	Sequence 373, App
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44	1706	100.0	1706	15	US-10-015-610A-373	Sequence 373, App
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46	1706	100.0	1706	15	US-10-012-752A-373	Sequence 373, App
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48	1706	100.0	1706	15	US-10-013-910A-373	Sequence 373, App
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58	1706	100.0	1706	15	US-10-012-753A-373	Sequence 373, App
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66	1706	100.0	1706	16	US-10-006-746A-373	Sequence 373, App
67	1706	100.0	1706	16	US-10-011-795A-373	Sequence 373, App
68	1706	100.0	1706	16	US-10-012-231A-373	Sequence 373, App
69	1706	100.0	1859	15	US-10-062-548-48	Sequence 48, Appl
70	1704.4	99.9	1765	15	US-10-037-270-705	Sequence 705, App
71	1704.4	99.9	1765	16	US-10-117-722-705	Sequence 705, App
72	1599.8	93.8	1688	13	US-09-823-245A-424	Sequence 424, App
73	1562.6	91.6	1715	15	US-10-062-548-59	Sequence 59, Appl
74	1022.2	59.9	1694	16	US-10-108-260A-2012	Sequence 2012, Ap
75	423.8	24.8	454	10	US-09-918-995-2481	Sequence 2481, Ap
76	403.8	23.7	407	10	US-09-918-995-6271	Sequence 6271, Ap
c 77	287.4	16.8	577	16	US-10-191-803-406	Sequence 406, App
78	287.2	16.8	292	13	US-10-085-783A-4907	Sequence 4907, Ap
79	287.2	16.8	292	16	US-10-242-535A-4907	Sequence 4907, Ap
80	285.6	16.7	324	9	US-09-736-457-942	Sequence 942, App
81	285.6	16.7	324	9	US-09-902-941-942	Sequence 942, App
82	285.6	16.7	324	9	US-09-849-626-942	Sequence 942, App
83	285.6	16.7	324	13	US-10-283-017-942	Sequence 942, App
84	285.6	16.7	324	15	US-10-017-754-942	Sequence 942, App
85	285.6	16.7	324	15	US-10-113-872-942	Sequence 942, App
86	148.8	8.7	170	13	US-10-085-783A-16426	Sequence 16426, A
87	148.8	8.7	170	16	US-10-242-535A-16426	Sequence 16426, A
88	148.8	8.7	1798	13	US-10-425-114-26974	Sequence 26974, A
c 89	143	8.4	1745	17	US-10-437-963-41350	Sequence 41350, A
90	142.8	8.4	400	9	US-09-783-590-5399	Sequence 5399, Ap
c 91	125.8	7.4	2165	17	US-10-437-963-85258	Sequence 85258, A
92	118.2	6.9	1933	13	US-10-424-599-87357	Sequence 87357, A
93	96.8	5.7	556	13	US-10-424-599-87354	Sequence 87354, A
94	95.8	5.6	1263	9	US-09-938-842A-1036	Sequence 1036, Ap
95	95.8	5.6	1263	11	US-09-938-842A-1036	Sequence 1036, Ap
96	90.8	5.3	653	17	US-10-021-323-1271	Sequence 1271, Ap
97	90.6	5.3	1398	13	US-10-425-114-17067	Sequence 17067, A
98	89.4	5.2	106	13	US-10-085-783A-23966	Sequence 23966, A
99	89.4	5.2	106	16	US-10-242-535A-23966	Sequence 23966, A
100	55.2	3.2	373	12	US-09-732-627A-2886	Sequence 2886, Ap
101	52.8	3.1	306	9	US-09-294-093B-5120	Sequence 5120, Ap
102	50.6	3.0	1320	13	US-10-425-114-5638	Sequence 5638, Ap
c 103	47.8	2.8	2357	13	US-10-027-632-110090	Sequence 110090,
c 104	47.8	2.8	2357	16	US-10-027-632-110090	Sequence 110090,
105	46	2.7	363	12	US-09-732-627A-625	Sequence 625, App
106	44.4	2.6	68233	16	US-10-034-650-31	Sequence 31, Appl
107	43	2.5	3594	17	US-10-437-963-51978	Sequence 51978, A
c 108	42.6	2.5	3489	13	US-09-894-273-1	Sequence 1, Appli
c 109	42.6	2.5	3489	15	US-10-294-804-1	Sequence 1, Appli
c 110	42.2	2.5	2049	17	US-10-437-963-87630	Sequence 87630, A
c 111	42.2	2.5	2236	17	US-10-437-963-87634	Sequence 87634, A
c 112	42	2.5	548	13	US-10-424-599-119959	Sequence 119959,

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OM nucleic - nucleic search, using sw model

Run on: August 6, 2004, 23:50:52 ; Search time 146 Seconds
                                            (without alignments)
                                            6484.563 Million cell updates/sec

Title: US-10-020-063A-373
Perfect score: 1706
Sequence: 1 ggagcgctgctggaacccga..........aaatgatcaaaaaaaaaaaa 1706

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1000 summaries

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     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result   Query
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      1   1706 100.0   1859 4 US-09-369-247-48   Sequence 48, Appl
      2 1704.4   99.9   1765 4 US-09-620-312D-705   Sequence 705, App
      3 1562.6   91.6   1715 4 US-09-369-247-59   Sequence 59, Appl
      4 285.6   16.7   324 4 US-09-702-705-942   Sequence 942, App
      5 285.6   16.7   324 4 US-09-736-457-942   Sequence 942, App
      6 285.6   16.7   324 4 US-09-614-124B-942   Sequence 942, App
      7 285.6   16.7   324 4 US-09-671-325-942   Sequence 942, App
      8   70   4.1   7218 1 US-08-232-463-14   Sequence 14, Appl
  c   9   42.6   2.5   3489 2 US-08-728-323A-1   Sequence 1, Appli
  c 10   42.6   2.5   3489 4 US-09-298-568-1   Sequence 1, Appli
  c 11   42.6   2.5   3489 4 US-09-410-399-1   Sequence 1, Appli